

SEQUENCE LISTING

<110> Meyers, Rachel E.
Millennium Pharmaceuticals Inc

<120> 33449, A Human Protease Family Member
and Uses Therefor

<130> MPI2001-016P1RCP1(M)

<150> 60/262,513
<151> 2001-01-18

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 721
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (115)...(615)

<400> 1
ccacgcgtcc gcttcggcgg ggcccagggtg agaaaggccc acctgtgtcc tggttgaggg 60
tctccagggt tctttggggc tcgaggccaa tgggtggcaga gtctacatag aact atg 117
Met
1

ctt cgt ggt gtt ctg ggg aaa acc ttt cga ctt gtt ggc tat act att 165
Leu Arg Gly Val Leu Gly Lys Thr Phe Arg Leu Val Gly Tyr Thr Ile
5 10 15

caa tat ggc tgt ata gct cat tgt gct ttt gaa tac gtt ggt ggt gtt 213
Gln Tyr Gly Cys Ile Ala His Cys Ala Phe Glu Tyr Val Gly Gly Val
20 25 30

gtc atg tgt tct gga cca tca atg gag cct aca att caa aat tca gat 261
Val Met Cys Ser Gly Pro Ser Met Glu Pro Thr Ile Gln Asn Ser Asp
35 40 45

att gtc ttt gca gaa aat ctt agt cga cat ttt tat ggt atc caa aga 309
Ile Val Phe Ala Glu Asn Leu Ser Arg His Phe Tyr Gly Ile Gln Arg
50 55 60 65

ggg gac att gtg att gca aaa agc cca agt gat cca aaa tca aat att 357
Gly Asp Ile Val Ile Ala Lys Ser Pro Ser Asp Pro Lys Ser Asn Ile
70 75 80

tgt aaa aga gta att ggt ttg gaa gga gac aaa atc ctc acc act agt 405
Cys Lys Arg Val Ile Gly Leu Glu Gly Asp Lys Ile Leu Thr Thr Ser
85 90 95

cca tca gat ttc ttt aaa agc cat agt tat gtg cca atg ggt cat gtt 453
Pro Ser Asp Phe Phe Lys Ser His Ser Tyr Val Pro Met Gly His Val
100 105 110

tgg tta gaa ggt gac aat cta cag aat tct aca gat tcc agg tgc tat 501
Trp Leu Glu Gly Asp Asn Leu Gln Asn Ser Thr Asp Ser Arg Cys Tyr
115 120 125

gga cct att cca tat gga cta ata aga gga cga atc ttc ttt aag att 549
Gly Pro Ile Pro Tyr Gly Leu Ile Arg Gly Arg Ile Phe Phe Lys Ile
130 135 140 145

tgg cct ctg agt gat ttt gga ttt tta cgt gcc agc cct aat ggc cac 597
Trp Pro Leu Ser Asp Phe Gly Phe Leu Arg Ala Ser Pro Asn Gly His
150 155 160

aga ttt tct gat gat tag taagcattta tctcttttgac ttgattattg 645
Arg Phe Ser Asp *
165

tctccttttc atgtgaattt attactcccg ttgaaaccgt gtacttacca ataaactatt 705
tgctattcaa aaaaaa 721

<210> 2
<211> 166
<212> PRT
<213> homo sapiens

<400> 2
Met Leu Arg Gly Val Leu Gly Lys Thr Phe Arg Leu Val Gly Tyr Thr
1 5 10 15
Ile Gln Tyr Gly Cys Ile Ala His Cys Ala Phe Glu Tyr Val Gly Gly
20 25 30
Val Val Met Cys Ser Gly Pro Ser Met Glu Pro Thr Ile Gln Asn Ser
35 40 45
Asp Ile Val Phe Ala Glu Asn Leu Ser Arg His Phe Tyr Gly Ile Gln
50 55 60
Arg Gly Asp Ile Val Ile Ala Lys Ser Pro Ser Asp Pro Lys Ser Asn
65 70 75 80
Ile Cys Lys Arg Val Ile Gly Leu Glu Gly Asp Lys Ile Leu Thr Thr
85 90 95
Ser Pro Ser Asp Phe Phe Lys Ser His Ser Tyr Val Pro Met Gly His
100 105 110
Val Trp Leu Glu Gly Asp Asn Leu Gln Asn Ser Thr Asp Ser Arg Cys
115 120 125
Tyr Gly Pro Ile Pro Tyr Gly Leu Ile Arg Gly Arg Ile Phe Phe Lys
130 135 140
Ile Trp Pro Leu Ser Asp Phe Gly Phe Leu Arg Ala Ser Pro Asn Gly
145 150 155 160
His Arg Phe Ser Asp Asp
165

<210> 3
<211> 501
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (1)...(501)

<400> 3
atg ctt cgt ggt gtt ctg ggg aaa acc ttt cga ctt gtt ggc tat act 48
Met Leu Arg Gly Val Leu Gly Lys Thr Phe Arg Leu Val Gly Tyr Thr

1	5	10	15	
att caa tat ggc tgt ata gct cat tgt gct ttt gaa tac gtt ggt ggt				96
Ile Gln Tyr Gly Cys Ile Ala His Cys Ala Phe Glu Tyr Val Gly Gly	20	25	30	
ggt gtc atg tgt tct gga cca tca atg gag cct aca att caa aat tca				144
Val Val Met Cys Ser Gly Pro Ser Met Glu Pro Thr Ile Gln Asn Ser	35	40	45	
gat att gtc ttt gca gaa aat ctt agt cga cat ttt tat ggt atc caa				192
Asp Ile Val Phe Ala Glu Asn Leu Ser Arg His Phe Tyr Gly Ile Gln	50	55	60	
aga ggt gac att gtg att gca aaa agc cca agt gat cca aaa tca aat				240
Arg Gly Asp Ile Val Ile Ala Lys Ser Pro Ser Asp Pro Lys Ser Asn	65	70	75	80
att tgt aaa aga gta att ggt ttg gaa gga gac aaa atc ctc acc act				288
Ile Cys Lys Arg Val Ile Gly Leu Glu Gly Asp Lys Ile Leu Thr Thr	85	90	95	
agt cca tca gat ttc ttt aaa agc cat agt tat gtg cca atg ggt cat				336
Ser Pro Ser Asp Phe Phe Lys Ser His Ser Tyr Val Pro Met Gly His	100	105	110	
ggt tgg tta gaa ggt gac aat cta cag aat tct aca gat tcc agg tgc				384
Val Trp Leu Glu Gly Asp Asn Leu Gln Asn Ser Thr Asp Ser Arg Cys	115	120	125	
tat gga cct att cca tat gga cta ata aga gga cga atc ttc ttt aag				432
Tyr Gly Pro Ile Pro Tyr Gly Leu Ile Arg Gly Arg Ile Phe Phe Lys	130	135	140	
att tgg cct ctg agt gat ttt gga ttt tta cgt gcc agc cct aat ggc				480
Ile Trp Pro Leu Ser Asp Phe Gly Phe Leu Arg Ala Ser Pro Asn Gly	145	150	155	160
cac aga ttt tct gat gat tag				501
His Arg Phe Ser Asp Asp *	165			

<210> 4

<211> 74

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus

<400> 4

Gly Gly Ser Met Glu Pro Thr Leu His Asp Thr Gly Asp Arg Leu Phe				
1	5	10	15	
Val Asn Lys Phe Leu Tyr Gly Ile Lys Leu Pro Val Ile Asp Lys Thr				
20	25	30		
Val Lys Asn Thr Gly Gly Ile Lys Arg Gly Asp Ile Val Val Phe Lys				
35	40	45		
Ala Pro Thr Lys Pro Asn Val His Tyr Val Lys Arg Val Ile Gly Leu				
50	55	60		
Pro Gly Asp Thr Val Lys Met Lys Asn Asp				

65

70

<210> 5
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus

<400> 5
 Gly Asp Asn Arg Leu Asn Ser Met Asp Ser Arg Tyr Gly Leu Gly Leu
 1 5 10 15
 Val Ala Leu Lys Asn Ile Val Gly
 20

<210> 6
 <211> 189
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 6
 Thr Val Gly Thr Leu Pro Ile Trp Ser Lys Thr Phe Ser Tyr Ala Ile
 1 5 10 15
 Arg Ser Leu Cys Phe Leu His Ile Ile His Met Tyr Ala Tyr Glu Phe
 20 25 30
 Thr Glu Thr Arg Gly Glu Ser Met Leu Pro Thr Leu Ser Ala Thr Asn
 35 40 45
 Asp Tyr Val His Val Leu Lys Asn Phe Gln Asn Gly Arg Gly Ile Lys
 50 55 60
 Met Gly Asp Cys Ile Val Ala Leu Lys Pro Thr Asp Pro Asn His Arg
 65 70 75 80
 Ile Cys Lys Arg Val Thr Gly Met Pro Gly Asp Leu Val Leu Val Asp
 85 90 95
 Pro Ser Thr Ile Val Asn Tyr Val Gly Asp Val Leu Val Asp Glu Glu
 100 105 110
 Arg Phe Gly Thr Tyr Ile Lys Val Pro Glu Gly His Val Trp Val Thr
 115 120 125
 Gly Asp Asn Leu Ser His Ser Leu Asp Ser Arg Thr Tyr Asn Ala Leu
 130 135 140
 Pro Met Gly Leu Ile Met Gly Lys Ile Val Ala Ala Asn Asn Phe Asp
 145 150 155 160
 Lys Pro Phe Trp Asp Gly Ser Ile Arg Asn Ile Trp Gly Phe Lys Trp
 165 170 175
 Ile Asn Asn Thr Phe Leu Asp Val Gln Ala Lys Ser Asn
 180 185

<210> 7
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus

<400> 7
 Arg Arg Gly Asp Leu
 1 5

1004543.011402

<210> 8
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> consensus

 <221> VARIANT
 <222> 1,2
 <223> The amino acid residue at positions 1 or 2 can be
 Leu, Ile, Val, Met, Phe, Tyr, or Trp.

 <221> VARIANT
 <222> 3,4,8-10,12,13
 <223> The amino acid residue at positions 3, 4, 8-10, 12
 and 13 can be any amino acid.

 <221> VARIANT
 <222> 7
 <223> The amino acid residue at position 7 can be Asn or
 His.

 <221> VARIANT
 <222> 11
 <223> The amino acid residue at position 11 can be Ser,
 Asn, or Asp.

 <221> VARIANT
 <222> 14
 <223> The amino acid residue at position 14 can be Ser
 or Gly.

 <400> 8
 Xaa Xaa Xaa Xaa Gly Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10

 <210> 9
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> consensus

 <221> VARIANT
 <222> 1
 <223> The amino acid residue at position 1 can be Gly or
 Ser.

 <221> VARIANT
 <222> 2,5
 <223> The amino acid residue at positions 2 and 5 can be
 any amino acid.

 <221> VARIANT
 <222> 6
 <223> The amino acid residue at position 6 can be Pro or

Ser.

<221> VARIANT

<222> 7

<223> The amino acid residue at position 7 can be Ala or Thr.

<221> VARIANT

<222> 8

<223> The amino acid residue at position 8 can be Leu or Phe.

<400> 9

Xaa Xaa Ser Met Xaa Xaa Xaa Xaa

1

5

<210> 10

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus

<221> VARIANT

<222> 3,4

<223> The amino acid residue at positions 3 or 4 can be Leu, Ile, Val, Met, Ser, Thr, or Ala.

<221> VARIANT

<222> 5

<223> The amino acid residue at position 5 can be Gly or Ala.

<221> VARIANT

<222> 6,10,12

<223> The amino acid residue at positions 6, 10, and 12 can be any amino acid.

<221> VARIANT

<222> 7

<223> The amino acid residue at position 7 can be Pro or Gly.

<221> VARIANT

<222> 9

<223> The amino acid residue at position 9 can be Asp or Glu.

<221> VARIANT

<222> (11)

<223> The amino acid residue at position 11 can be Leu, Ile, Val, or Met.

<221> VARIANT

<222> (13)

<223> The amino acid residue at position 13 can be Leu, Ile, Val, Met, Phe, or Tyr.

<400> 10

Lys	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10			

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